

#2

PCT10

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/018,386

DATE: 01/09/2002
 TIME: 12:13:24

Input Set : A:\MSB-7268.txt
 Output Set: N:\CRF3\01082002\J018386.raw

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3 <110> APPLICANT: Bayer AG
 4 Friedrich, Gabi
 5 Hagen, Gustav
 6 Wick, Maresa
 7 Zubov, Dmitry
 8 Dubois-Stringfellow, Nathalie A.
 10 <120> TITLE OF INVENTION: METHODS FOR MODULATING ANGIOGENESIS
 12 <130> FILE REFERENCE: 17956A-000500PC
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/018,386
 C--> 15 <141> CURRENT FILING DATE: 2001-12-13
 17 <150> PRIOR APPLICATION NUMBER: EP 99113502.1
 18 <151> PRIOR FILING DATE: 1999-07-02
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
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 61 cccccctcctg acctctcgta gccattgcca ggagccacc ctggtcacgc tggccacagc 1920
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 63 gtttccgaa gtcactgcag cggatgatgg aactgaatcg atacggtgtt ttctgtccct 2040
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 79 20 25 30
 81 Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys Arg Ala Gly
 82 35 40 45
 84 Glu Ser Gln Asp Lys Cys Thr Tyr Thr Phe Ile Val Pro Gln Gln Arg
 85 50 55 60
 87 Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu Pro Glu Val Leu Leu
 88 65 70 75 80
 90 Glu Asn Arg Val His Lys Gln Glu Leu Glu Leu Leu Asn Asn Glu Leu
 91 85 90 95
 93 Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu Gln Gln Leu Val Lys Val
 94 100 105 110
 96 Asp Gly Gly Ile Val Ser Glu Val Lys Leu Leu Arg Lys Glu Ser Arg
 97 115 120 125
 99 Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu
 100 130 135 140
 102 Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn
 103 145 150 155 160
 105 Arg Ile Leu Asn Gln Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr
 106 165 170 175
 108 Lys Asp Leu Glu His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn
 109 180 185 190
 111 Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro
 112 195 200 205
 114 Ser Ala Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val
 115 210 215 220
 117 Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
 118 225 230 235 240
 120 Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro
 121 245 250 255
 123 Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser
 124 260 265 270
 126 Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly His Asp Thr

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127	275	280	285
129	Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg Leu Met Gln		
130	290	295	300
132	Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln		
133	305	310	315
135	Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr		320
136	325	330	335
138	Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu		
139	340	345	350
141	Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr		
142	355	360	365
144	Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe		
145	370	375	380
147	Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr		
148	385	390	395
150	His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe		400
151	405	410	415
153	Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His		
154	420	425	430
156	Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu		
157	435	440	445
159	Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp		
160	450	455	460
162	Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys		
163	465	470	475
165	Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His		480
166	485	490	
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170	<211> LENGTH: 498		
171	<212> TYPE: PRT		
172	<213> ORGANISM: Homo sapiens		
174	<400> SEQUENCE: 3		
175	Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His		
176	1	5	10
			15
178	Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg		
179	20	25	30
181	Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro		
182	35	40	45
184	Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr		
185	50	55	60
187	Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser		
188	65	70	75
			80
190	Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp		
191	85	90	95
193	Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met		
194	100	105	110
196	Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu		
197	115	120	125
199	Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys		

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202	Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu		
203	145	150	155
205	Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln		160
206	165	170	175
208	Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser		
209	180	185	190
211	Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu		
212	195	200	205
214	Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr		
215	210	215	220
217	Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala		
218	225	230	235
220	Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp		240
221	245	250	255
223	Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu		
224	260	265	270
226	Lys Gly Gly Lys Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp		
227	275	280	285
229	Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile		
230	290	295	300
232	Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn		
233	305	310	315
235	Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp		320
236	325	330	335
238	Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser		
239	340	345	350
241	Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln		
242	355	360	365
244	Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg		
245	370	375	380
247	Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn		
248	385	390	395
250	Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser		400
251	405	410	415
253	Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn		
254	420	425	430
256	Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp		
257	435	440	445
259	Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala		
260	450	455	460
262	Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys		
263	465	470	475
265	Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu		480
266	485	490	495
268	Asp Phe		
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273	<211> LENGTH: 496		
274	<212> TYPE: PRT		

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275 <213> ORGANISM: Homo sapiens
 277 <400> SEQUENCE: 4
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 20 25 30
 284 Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
 35 40 45
 287 Glu Met Asp Asn Cys Arg Ser Ser Ser Pro Tyr Val Ser Asn Ala
 50 55 60
 290 Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
 65 70 75 80
 293 Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
 85 90 95
 296 Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
 100 105 110
 299 Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
 115 120 125
 302 Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
 130 135 140
 305 Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
 145 150 155 160
 308 Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
 165 170 175
 311 Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
 180 185 190
 314 Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
 195 200 205
 317 Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
 210 215 220
 320 Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn
 225 230 235 240
 323 Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
 245 250 255
 326 Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
 260 265 270
 329 Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
 275 280 285
 332 Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
 290 295 300
 335 Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
 305 310 315 320
 338 Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
 325 330 335
 341 Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
 340 345 350
 344 Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
 355 360 365
 347 Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr

VERIFICATION SUMMARY

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Input Set : A:\MSB-7268.txt

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date